

Abstract

The level of genetic relatedness or dissimilarity of Lablab genotypes used by growers in different regions in Kenya has not been determined. In this study, ninety six (96) Lablab accessions collected from various parts of Kenya were characterized based on simple sequence repeat (SSR) molecular markers. Ten SSR primers were used and detected a mean of 4.3 alleles per primer. Expected heterozygosity was on average 0.38. The average polymorphic information content (PIC) was 0.63. Analysis of molecular variance (AMOVA) revealed 15% genetic variation among populations and 85% variation within populations. Highest Nei's genetic distance of 0.998 was found between Western and Mwingi populations while lowest genetic distance of 0.092 was found between Embu and Meru populations. Lablab purpureus populations exhibited a high level of relatedness as revealed by cluster analysis and dendrogram based unweighted pair group method with arithmetic averages (UPGMA)